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RAW SEQUENCE LISTING

DATE: 03/27/2002

PATENT APPLICATION: US/10/092,640

TIME: 14:24:25

Input Set : A:\407T-897221US seq list.txt

Output Set: N:\CRF3\03272002\J092640.raw

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Marks, James D.
7           Schier, Robert
9   (ii) TITLE OF INVENTION: Novel High Affinity Human Antibodies to
10          Tumor Antigens
12  (iii) NUMBER OF SEQUENCES: 141
14  (iv) CORRESPONDENCE ADDRESS:
15      (A) ADDRESSEE: Quine Intellectual Property Law Group P.C.
16      (B) STREET: 2033 Clement Ave. Suite 200
17      (C) CITY: Alameda
18      (D) STATE: California
19      (E) COUNTRY: USA
20      (F) ZIP: 94501
22  (v) COMPUTER READABLE FORM:
23      (A) MEDIUM TYPE: Floppy disk
24      (B) COMPUTER: IBM PC compatible
25      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28  (vi) CURRENT APPLICATION DATA:
C--> 29      (A) APPLICATION NUMBER: US/10/092,640
C--> 30      (B) FILING DATE: 05-Mar-2002
31      (C) CLASSIFICATION:
45  (vii) PRIOR APPLICATION DATA:
34      (A) APPLICATION NUMBER: US 60/000,238
35      (B) FILING DATE: 14-JUN-1995
38      (A) APPLICATION NUMBER: US 60/000,250
39      (B) FILING DATE: 15-JUN-1995
42      (A) APPLICATION NUMBER: US 08/665,202
43      (B) FILING DATE: 13-JUN-1996
46      (A) APPLICATION NUMBER: US 09/315,574
47      (B) FILING DATE: 20-MAY-1999
49  (viii) ATTORNEY/AGENT INFORMATION:
50      (A) NAME: Hunter, Tom
51      (B) REGISTRATION NUMBER: 38,498
52      (C) REFERENCE/DOCKET NUMBER: 02307E-061411
54  (ix) TELECOMMUNICATION INFORMATION:
55      (A) TELEPHONE: (415) 576-0200
56      (B) TELEFAX: (415) 576-0300
59 (2) INFORMATION FOR SEQ ID NO: 1:
61   (i) SEQUENCE CHARACTERISTICS:
62      (A) LENGTH: 15 amino acids
63      (B) TYPE: amino acid

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64          (C) STRANDEDNESS:
65          (D) TOPOLOGY: linear
67      (ii) MOLECULE TYPE: peptide
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72      Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
73      1          5          10          15
76 (2) INFORMATION FOR SEQ ID NO: 2:
78      (i) SEQUENCE CHARACTERISTICS:
79          (A) LENGTH: 5 amino acids
80          (B) TYPE: amino acid
81          (C) STRANDEDNESS:
82          (D) TOPOLOGY: linear
84      (ii) MOLECULE TYPE: peptide
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
89      Ser Ser Ser Ser Gly
90      1          5
93 (2) INFORMATION FOR SEQ ID NO: 3:
95      (i) SEQUENCE CHARACTERISTICS:
96          (A) LENGTH: 15 amino acids
97          (B) TYPE: amino acid
98          (C) STRANDEDNESS:
99          (D) TOPOLOGY: linear
101     (ii) MOLECULE TYPE: peptide
104     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
106     Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
107     1          5          10          15
110 (2) INFORMATION FOR SEQ ID NO: 4:
112     (i) SEQUENCE CHARACTERISTICS:
113         (A) LENGTH: 774 base pairs
114         (B) TYPE: nucleic acid
115         (C) STRANDEDNESS: single
116         (D) TOPOLOGY: linear
W--> 118     (ii) MOLECULE TYPE: DNA
121     (ix) FEATURE:
122         (A) NAME/KEY: CDS
123         (B) LOCATION: 1..774
124         (D) OTHER INFORMATION: /note= "sequence of C6 sFv
125 antibody C6.5"
128     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
130 CAG GTG CAG CTG TTG CAG TCT GGG GCA GAG TTG AAA AAA CCC GGG GAG      48
131 Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
132 1          5          10          15
134 TCT CTG AAG ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC AGC TAC      96
135 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
136          20          25          30
138 TGG ATC GCC TGG GTG CGC CAG ATG CCC GGG AAA GGC CTG GAG TAC ATG      144
139 Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
140          35          40          45
142 GGG CTC ATC TAT CCT GGT GAC TCT GAC ACC AAA TAC AGC CCG TCC TTC      192

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143 Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
144      50      55      60
146 CAA GGC CAG GTC ACC ATC TCA GTC GAC AAG TCC GTC AGC ACT GCC TAC      240
147 Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
148 65      70      75      80
150 TTG CAA TGG AGC AGT CTG AAG CCC TCG GAC AGC GCC GTG TAT TTT TGT      288
151 Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
152      85      90      95
154 GCG AGA CAT GAC GTG GGA TAT TGC AGT AGT TCC AAC TGC GCA AAG TGG      336
155 Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
156      100      105      110
158 CCT GAA TAC TTC CAG CAT TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC      384
159 Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
160      115      120      125
162 TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC GGT GGC GGA TCG      432
163 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
164      130      135      140
166 CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GCG GCC CCA GGA CAG      480
167 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
168 145      150      155      160
170 AAG GTC ACC ATC TCC TGC TCT GGA AGC AGC TCC AAC ATT GGG AAT AAT      528
171 Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
172      165      170      175
174 TAT GTA TCC TGG TAC CAG CAG CTC CCA GGA ACA GCC CCC AAA CTC CTC      576
175 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
176      180      185      190
178 ATC TAT GGT CAC ACC AAT CGG CCC GCA GGG GTC CCT GAC CGA TTC TCT      624
179 Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
180      195      200      205
182 GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG TTC CGG      672
183 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg
184      210      215      220
186 TCC GAG GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG      720
187 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
188 225      230      235      240
190 AGT GGT TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG      768
191 Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
192      245      250      255
194 GCC GCA      774
195 Ala Ala
198 (2) INFORMATION FOR SEQ ID NO: 5:
200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 258 amino acids
202 (B) TYPE: amino acid
203 (D) TOPOLOGY: linear
205 (ii) MOLECULE TYPE: protein
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209 Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
210 1      5      10      15

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212 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
213                20                25                30
215 Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
216                35                40                45
218 Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
219                50                55                60
221 Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
222 65                70                75                80
224 Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
225                85                90                95
227 Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
228                100               105               110
230 Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
231                115               120               125
233 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
234 130               135               140
236 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
237 145               150               155               160
239 Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
240                165               170               175
242 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
243                180               185               190
245 Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
246                195               200               205
248 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg
249                210               215               220
251 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
252 225               230               235               240
254 Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala
255                245               250               255
257 Ala Ala

```

260 (2) INFORMATION FOR SEQ ID NO: 6:

262 (i) SEQUENCE CHARACTERISTICS:

263 (A) LENGTH: 11 amino acids

264 (B) TYPE: amino acid

265 (C) STRANDEDNESS:

266 (D) TOPOLOGY: linear

268 (ii) MOLECULE TYPE: peptide

271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

273 Ala Ala Trp Asp Asp Ser Leu Ser Gly Trp Val

274 1 5 10

277 (2) INFORMATION FOR SEQ ID NO: 7:

279 (i) SEQUENCE CHARACTERISTICS:

280 (A) LENGTH: 11 amino acids

281 (B) TYPE: amino acid

282 (C) STRANDEDNESS:

283 (D) TOPOLOGY: linear

285 (ii) MOLECULE TYPE: peptide

288 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

RAW SEQUENCE LISTING

DATE: 03/27/2002

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TIME: 14:24:25

Input Set : A:\407T-897221US seq list.txt

Output Set: N:\CRF3\03272002\J092640.raw

290 Ala Ala Trp Asp Tyr Ser Leu Ser Gly Trp Val
291 1 5 10

294 (2) INFORMATION FOR SEQ ID NO: 8:

296 (i) SEQUENCE CHARACTERISTICS:

297 (A) LENGTH: 11 amino acids

298 (B) TYPE: amino acid

299 (C) STRANDEDNESS:

300 (D) TOPOLOGY: linear

302 (ii) MOLECULE TYPE: peptide

305 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

307 Ala Ala Trp Asp His Ser Leu Ser Gly Trp Val
308 1 5 10

311 (2) INFORMATION FOR SEQ ID NO: 9:

313 (i) SEQUENCE CHARACTERISTICS:

314 (A) LENGTH: 11 amino acids

315 (B) TYPE: amino acid

316 (C) STRANDEDNESS:

317 (D) TOPOLOGY: linear

319 (ii) MOLECULE TYPE: peptide

322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

324 Ala Ser Trp Asp Tyr Ser Leu Ser Gly Trp Val
325 1 5 10

328 (2) INFORMATION FOR SEQ ID NO: 10:

330 (i) SEQUENCE CHARACTERISTICS:

331 (A) LENGTH: 11 amino acids

332 (B) TYPE: amino acid

333 (C) STRANDEDNESS:

334 (D) TOPOLOGY: linear

336 (ii) MOLECULE TYPE: peptide

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

341 Ala Ala Trp Asp Tyr Ser Leu Trp Gly Trp Val
342 1 5 10

345 (2) INFORMATION FOR SEQ ID NO: 11:

347 (i) SEQUENCE CHARACTERISTICS:

348 (A) LENGTH: 11 amino acids

349 (B) TYPE: amino acid

350 (C) STRANDEDNESS:

351 (D) TOPOLOGY: linear

353 (ii) MOLECULE TYPE: peptide

356 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

358 Ala Thr Trp Asp Tyr Ala Leu Ser Gly Trp Val
359 1 5 10

362 (2) INFORMATION FOR SEQ ID NO: 12:

364 (i) SEQUENCE CHARACTERISTICS:

365 (A) LENGTH: 11 amino acids

366 (B) TYPE: amino acid

367 (C) STRANDEDNESS:

368 (D) TOPOLOGY: linear

370 (ii) MOLECULE TYPE: peptide

VERIFICATION SUMMARY

DATE: 03/27/2002

PATENT APPLICATION: US/10/092,640

TIME: 14:24:26

Input Set : A:\407T-897221US seq list.txt

Output Set: N:\CRF3\03272002\J092640.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:32
L:2021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
L:2734 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=110
L:2750 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=111
L:2766 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=112
L:2782 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=113
L:2798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=114
L:2814 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=115
L:2830 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=116
L:2846 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=117
L:2862 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=118
L:2878 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=119
L:2894 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=120
L:2910 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=121
L:2926 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=122
L:2942 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=123
L:2958 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=124
L:2976 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=125
L:2994 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=126
L:3010 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=127
L:3026 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=128
L:3042 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=129
L:3058 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=130
L:3074 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=131
L:3090 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=132
L:3106 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=133
L:3122 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=134
L:3140 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=135
L:3158 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=136
L:3176 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=137
L:3192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=138
L:3208 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=139
L:3224 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=140
L:3240 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=141